Figure 1

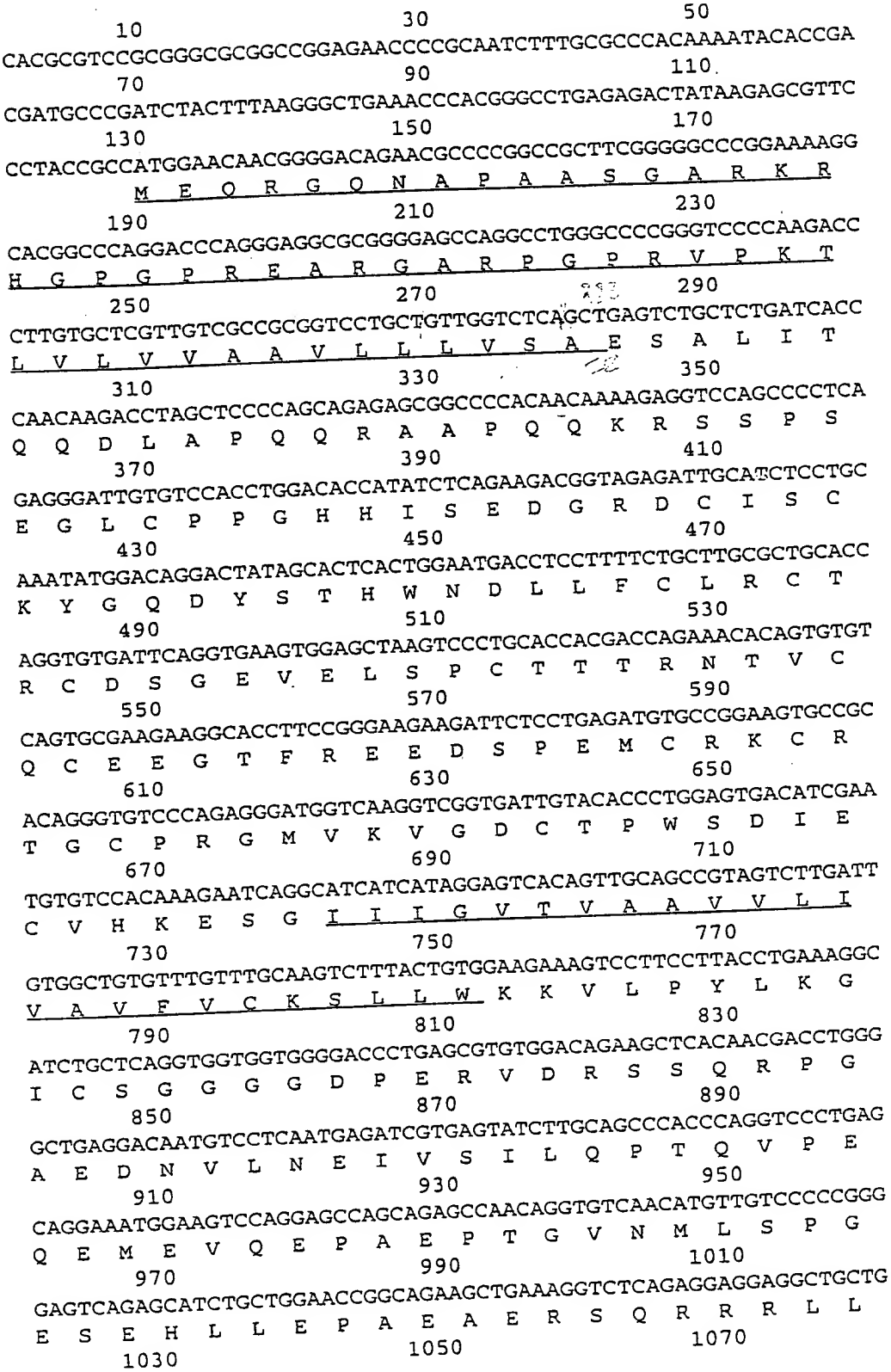
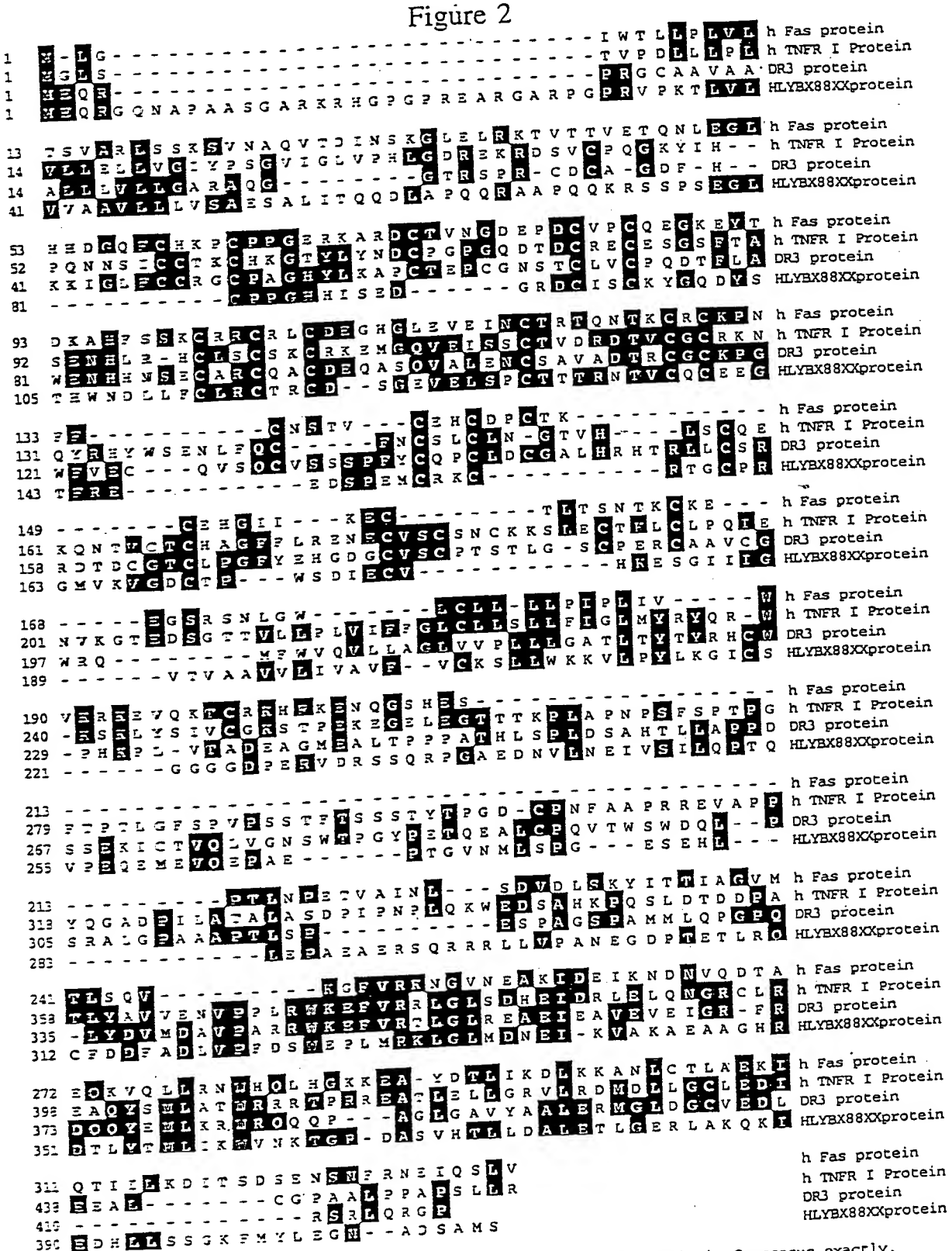

10 30 50
CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCCACAAAATACACCGA
70 90 110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
130 150 170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
M E Q R G Q N A P A A S G A R K R
190 210 230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
250 270 290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T
310 330 350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
Q Q D L A P Q Q R A A P Q Q K R S S P S
370 390 410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
E G L C P P G H H I S E D G R D C I S C
430 450 470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
K Y G Q D Y S T H W N D L L F C L R C T
490 510 530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
R C D S G E V E L S P C T T T R N T V C
550 570 590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
Q C E E G T F R E E D S P E M C R K C R
610 630 650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
T G C P R G M V K V G D C T P W S D I E
670 690 710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C V H K E S G I I I G V T V A A V V L I
730 750 770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
790 810 830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
I C S G G G G D P E R V D R S S Q R P G
850 870 890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A E D N V L N E I V S I L Q P T Q V P E
910 930 950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q E M E V Q E P A E P T G V N M L S P G
970 990 1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E S E H L L E P A E A E R S Q R R R L L
1030 1050 1070

Figure 1 (continued)

```
GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V   P   A   N   E   G   D   P   T   E   T   L   R   Q   C   F   D   D   F   A
        1090                       1110                        1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D   L   V   P   F   D   S   W   E   P   L   M   R   K   L   G   L   M   D   N
        1150                       1170                        1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E   I   K   V   A   K   A   E   A   A   G   H   R   D   T   L   Y   T   M   L
        1210                       1230                        1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I   K   W   V   N   K   T   G   R   D   A   S   V   H   T   L   L   D   A   L
        1270                       1290                        1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E   T   L   G   E   R   L   A   K   Q   K   I   E   D   H   L   L   S   S   G
        1330                       1350                        1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K   F   M   Y   L   E   G   N   A   D   S   A   M   S   *
        1390                       1410                        1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
        1450                       1470                        1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA
        1510                       1530                        1550
TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC
        1570                       1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA
```

Figure 2



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

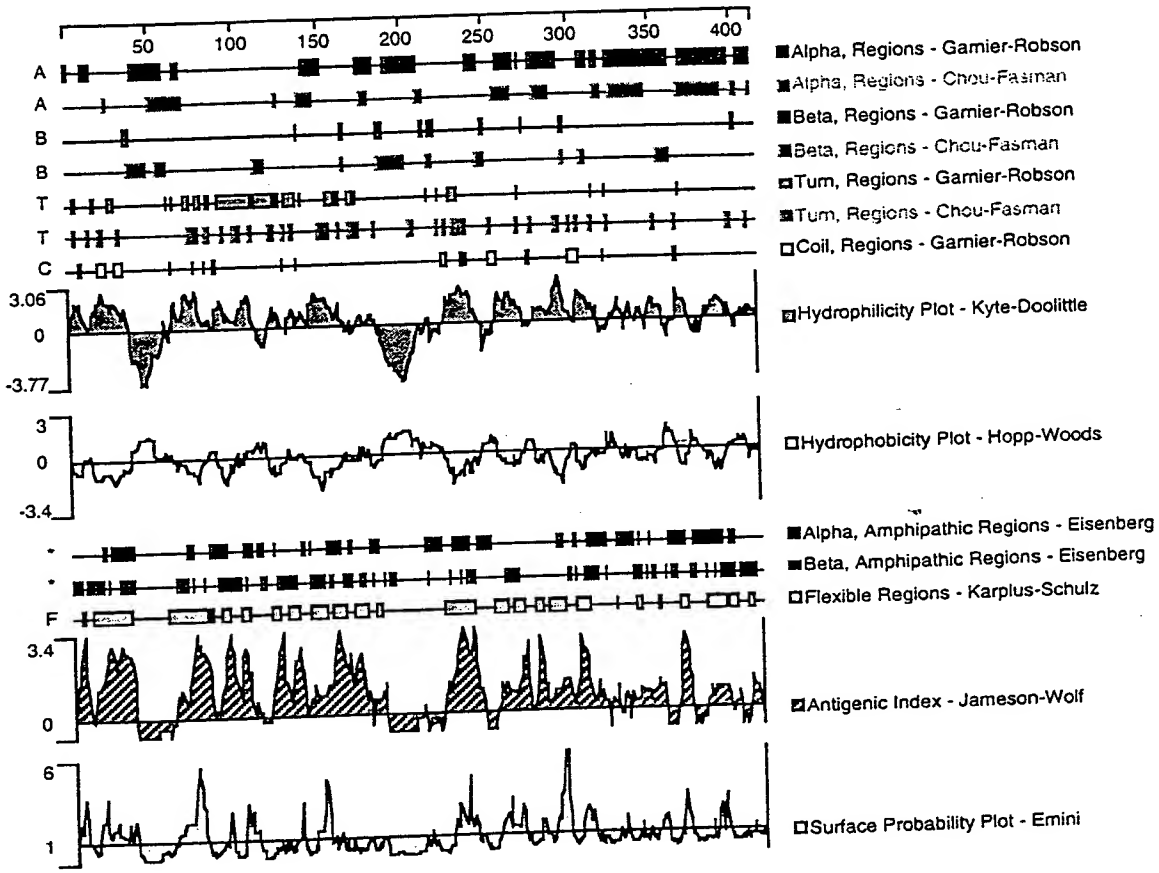

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
3.06
0
-3.77
3
0
-3.4
*
*
F
3.4
0
6
1
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

Figure 4

HAPBU13R

```
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG
```

HSBBU76R

```
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
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Figure 5

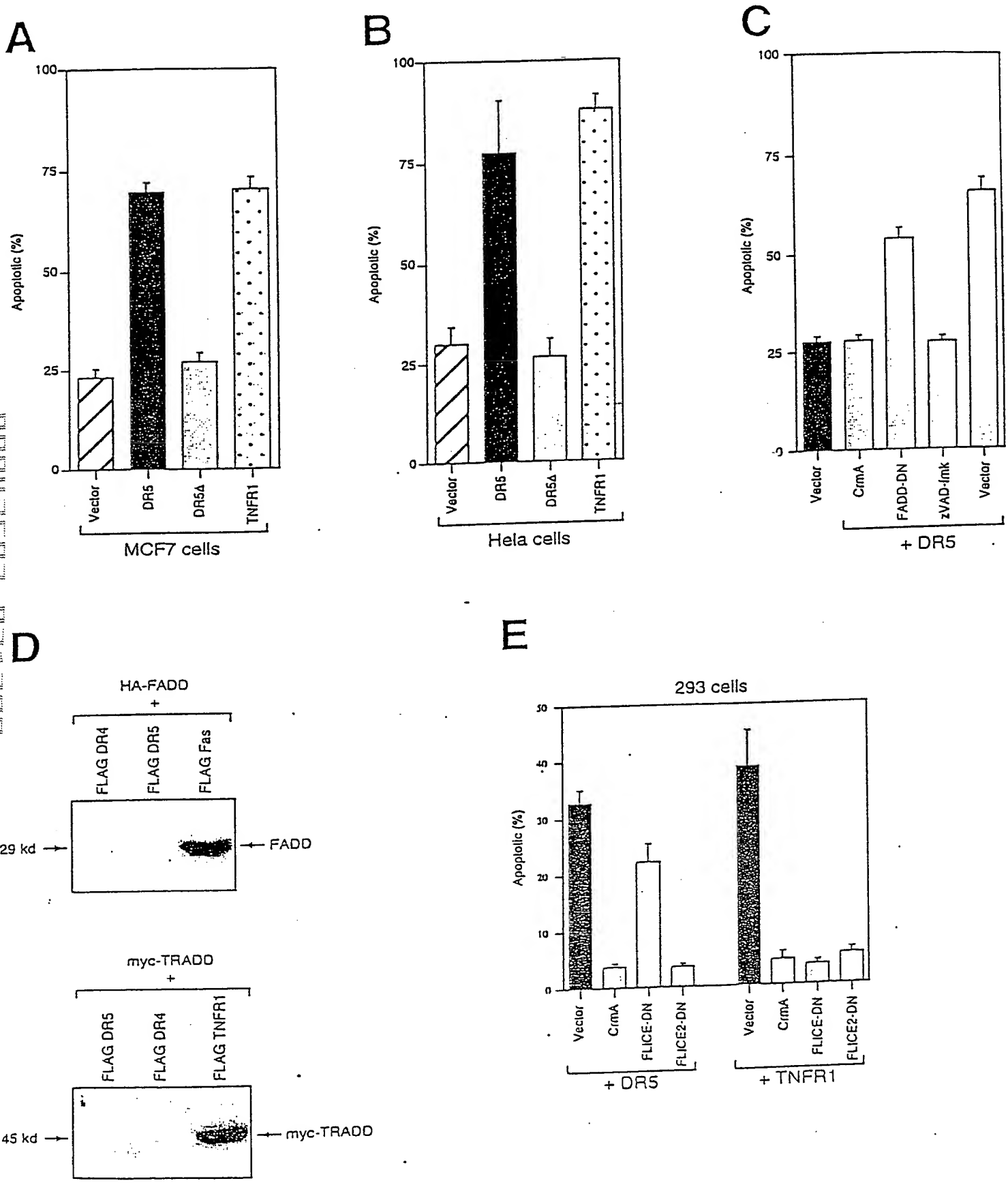
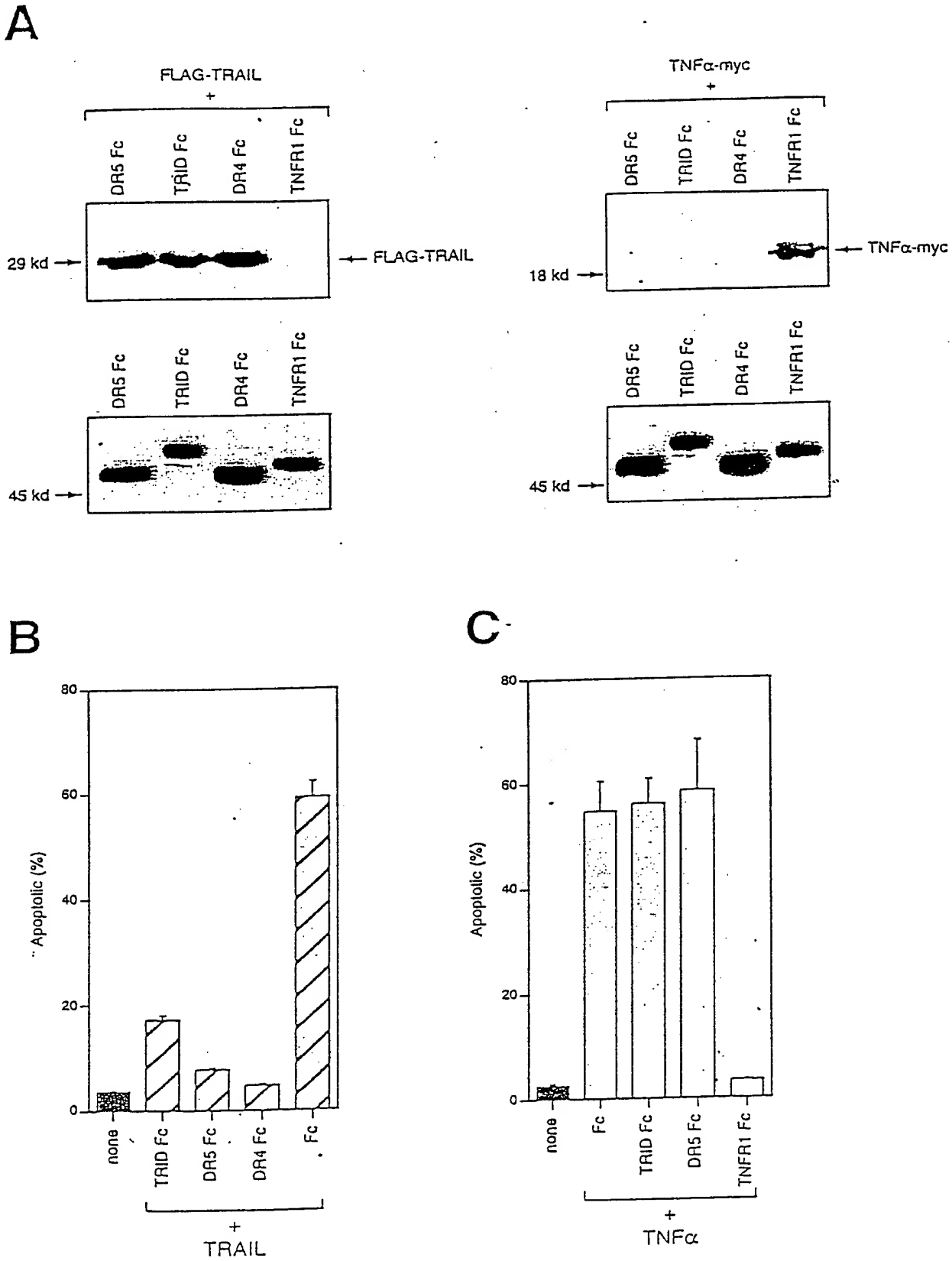

A
Apoptotic (%)
100
75
50
25
0
Vector
DR5
DR5Δ
TNFR1
MCF7 cells
B
Apoptotic (%)
100
75
50
25
0
Vector
DR5
DR5Δ
TNFR1
Hela cells
C
Apoptotic (%)
100
75
50
25
0
Vector
CrmA
FADD-DN
zVAD-fmk
Vector
+ DR5
D
HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD
myc-TRADD
+
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD
E
293 cells
Apoptotic (%)
50
40
30
20
10
0
Vector
CrmA
FLICE-DN
FLICE2-DN
Vector
CrmA
FLICE-DN
FLICE2-DN
+ DR5
+ TNFR1

Figure 6


A
FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
45 kd
TNFα-myc
18 kd
TNFα-myc
B
Apoptotic (%)
80
60
40
20
0
none
TRID Fc
DR5 Fc
DR4 Fc
Fc
+
TRAIL
C
Apoptotic (%)
80
60
40
20
0
none
Fc
TRID Fc
DR5 Fc
TNFR1 Fc
+
TNFα